

SEQUENCE LISTING

<110> Wood, Kenneth
 Finer, Jeffrey
 Beraud, Christophe
 Mak, John
 Sakowicz, Roman

<120> Methods of screening for modulators of
 cell proliferation and methods of diagnosing cell
 proliferation states

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<141> 1999-10-27

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<170> FastSEQ for Windows Version 4.0

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 65 70 75 80
 Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
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Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
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 Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
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 Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
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 Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser
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 Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val
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 atggataata aaaatgaact tgaccagtgt aaatctgacc tgcaaaataa aacacaagaa 1380
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 <212> PRT
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 Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
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 Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
 65 70 75 80
 Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
 85 90 95
 Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
 100 105 110
 Phe Thr Met Glu Gly Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu
 115 120 125
 Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
 130 135 140
 Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu
 145 150 155 160
 Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser
 165 170 175
 Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
 180 185 190
 Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp
 195 200 205
 Glu Val Tyr Gly Ile Leu Glu Lys Gly Ala Ala Lys Arg Thr Thr Ala
 210 215 220
 Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser

225 230 235 240
 Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val
 245 250 255
 Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Asn Ile
 260 265 270
 Gly Arg Ser Gly Ala Val Asp Lys Arg Ala Arg Glu Ala Gly Asn Ile
 275 280 285
 Asn Gln Ser Leu Leu Thr Leu Gly Arg Val Ile Thr Ala Leu Val Glu
 290 295 300
 Arg Thr Pro His Val Pro Tyr Arg Glu Ser Lys Leu Thr Arg Ile Leu
 305 310 315 320
 Gln Asp Ser Leu Gly Gly Arg Thr Arg Thr Ser Ile Ile Ala Thr Ile
 325 330 335
 Ser Pro Ala Ser Leu Asn Leu Glu Glu Thr Leu Ser Thr Leu Glu Tyr
 340 345 350
 Ala His Arg Ala Lys Asn Ile Leu Asn Lys Pro Glu Val Asn Gln Lys
 355 360 365
 Leu Thr Lys Lys Ala Leu Ile Lys Glu Tyr Thr Glu Glu Ile Glu Arg
 370 375 380
 Leu Lys Arg Asp Leu Ala Ala Arg Glu Lys Asn Gly Val Tyr Ile
 385 390 395 400
 Ser Glu Glu Asn Phe Arg Val Met Ser Gly Lys Leu Thr Val Gln Glu
 405 410 415
 Glu Gln Ile Val Glu Leu Ile Glu Lys Ile Gly Ala Val Glu Glu Glu
 420 425 430
 Leu Asn Arg Val Thr Glu Leu Phe Met Asp Asn Lys Asn Glu Leu Asp
 435 440 445
 Gln Cys Lys Ser Asp Leu Gln Asn Lys Thr Gln Glu Leu Glu Thr Thr
 450 455 460
 Gln Lys His Leu Gly Glu Thr Lys Leu Gly Leu Val Lys Glu Glu Tyr
 465 470 475 480
 Ile Thr Ser Ala Leu Glu Ser Thr Glu Glu Lys Leu His Asp Ala Ala
 485 490 495
 Ser Lys Leu Leu Asn Thr Val Glu Glu Thr Thr Lys Asp Val Ser Gly
 500 505 510
 Leu His Ser Lys Leu Asp Arg Lys Lys Ala Val Asp Gln His Asn Ala
 515 520 525
 Glu Ala Gln Asp Ile Phe Gly Lys Asn Leu Asn Ser Leu Phe Asn Asn
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 <213> Human

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 ttggagatct ataataaga gctttttgat ctcttaatc catcatctga tgtttctgag 540
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 gaaattacag tacacaacaa ggaatgaagt tatcaaattt tagaaaaggg ggcagcaaaa 660
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 caggattctc ttggagggcg tacaagaaca tctataattg caacaatttc tctgcatct 1020
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 Arg Lys Ala Ser Ala His Ser Ile Val Glu Cys Asp Pro Val Arg Lys
 35 40 45
 Glu Val Ser Val Arg Thr Gly Gly Leu Ala Asp Lys Ser Ser Arg Lys
 50 55 60
 Thr Tyr Thr Phe Asp Met Val Phe Gly Ala Ser Thr Lys Gln Ile Asp
 65 70 75 80
 Val Tyr Arg Ser Val Val Cys Pro Ile Leu Asp Glu Val Ile Met Gly
 85 90 95
 Tyr Asn Cys Thr Ile Phe Ala Tyr Gly Gln Thr Gly Thr Gly Lys Thr
 100 105 110
 Phe Thr Met Glu Gly Glu Arg Ser Pro Asn Glu Glu Tyr Thr Trp Glu
 115 120 125
 Glu Asp Pro Leu Ala Gly Ile Ile Pro Arg Thr Leu His Gln Ile Phe
 130 135 140
 Glu Lys Leu Thr Asp Asn Gly Thr Glu Phe Ser Val Lys Val Ser Leu
 145 150 155 160
 Leu Glu Ile Tyr Asn Glu Glu Leu Phe Asp Leu Leu Asn Pro Ser Ser
 165 170 175
 Asp Val Ser Glu Arg Leu Gln Met Phe Asp Asp Pro Arg Asn Lys Arg
 180 185 190
 Gly Val Ile Ile Lys Gly Leu Glu Glu Ile Thr Val His Asn Lys Asp
 195 200 205
 Glu Val Tyr Gly Ile Leu Glu Lys Gly Ala Ala Lys Arg Thr Thr Ala
 210 215 220
 Ala Thr Leu Met Asn Ala Tyr Ser Ser Arg Ser His Ser Val Phe Ser
 225 230 235 240
 Val Thr Ile His Met Lys Glu Thr Thr Ile Asp Gly Glu Glu Leu Val
 245 250 255
 Lys Ile Gly Lys Leu Asn Leu Val Asp Leu Ala Gly Ser Glu Asn Ile

	260		265		270	
Gly	Arg	Ser	Gly	Ala	Val	Asp
	275		280		285	
Asn	Gln	Ser	Leu	Leu	Thr	Leu
	290		295		300	
Arg	Thr	Pro	His	Val	Pro	Tyr
	305		310		315	
Gln	Asp	Ser	Leu	Gly	Gly	Arg
	325		330		335	
Ser	Pro	Ala	Ser	Leu	Asn	Leu
	340		345		350	
Ala	His	Arg	Ala	Lys	Asn	Ile
	355		360		365	

Lys Arg Ala Arg Glu Ala Gly Asn Ile
 Val Ile Thr Ala Leu Val Glu
 Arg Glu Ser Lys Leu Thr Arg Ile Leu
 Thr Arg Thr Ser Ile Ile Ala Thr Ile
 Glu Thr Leu Ser Thr Leu Glu Tyr
 Leu Asn Lys Pro Glu Val Asn Gln Lys